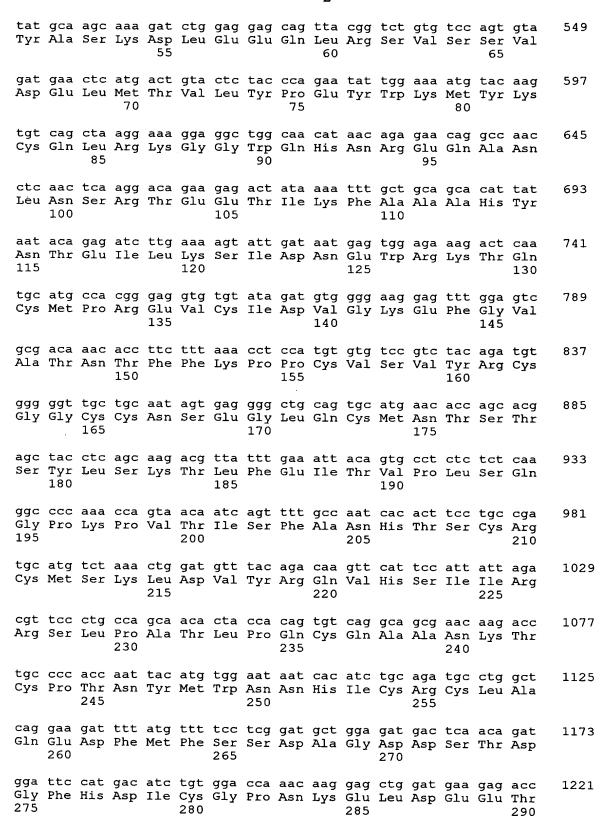SEQUENCE LISTING

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<110> Alitalo, Kari
      Ylä-Herttuala, Seppo
      Hiltunen, Mikko O
      Jeltsch, Markku M
      Achen, Marc G

<120> Use of VEGF-C or VEGF-D Gene or Protein to Prevent Restenosis

<130> 28967/35601A

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<150> US 60/105,587
<151> 1998-10-26

<160> 18

<170> PatentIn Ver. 2.0

<210> 1
<211> 1997
<212> DNA
<213> Homo sapiens

<220>
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<222> (352)..(1608)

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ggaacgcgga gccccggacc cgctcccgcc gcctccggct cgcccagggg gggtcgccgg 240

gaggagcccg ggggagaggg accaggaggg gcccgcggcc tcgcaggggc gcccgcgccc 300

ccacccctgc ccccgccagc ggaccggtcc cccacccccg tccttccac c atg cac 357
                                                        Met His
                                                          1

ttg ctg ggc ttc ttc tct gtg gcg tgt tct ctg ctc gcc gct gcg ctg   405
Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala Ala Leu
            5               10                  15

ctc ccg ggt cct cgc gag gcg ccc gcc gcc gcc gcc gcc ttc gag tcc   453
Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe Glu Ser
        20                  25                  30

gga ctc gac ctc tcg gac gcg gag ccc gac gcg ggc gag gcc acg gct   501
Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala Thr Ala
 35                 40                  45                  50
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tat gca agc aaa gat ctg gag gag cag tta cgg tct gtg tcc agt gta        549
Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val
                55                  60                  65

gat gaa ctc atg act gta ctc tac cca gaa tat tgg aaa atg tac aag        597
Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys
            70                  75                  80

tgt cag cta agg aaa gga ggc tgg caa cat aac aga gaa cag gcc aac        645
Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn
        85                  90                  95

ctc aac tca agg aca gaa gag act ata aaa ttt gct gca gca cat tat        693
Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr
    100                 105                 110

aat aca gag atc ttg aaa agt att gat aat gag tgg aga aag act caa        741
Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln
115                 120                 125                 130

tgc atg cca cgg gag gtg tgt ata gat gtg ggg aag gag ttt gga gtc        789
Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val
                135                 140                 145

gcg aca aac acc ttc ttt aaa cct cca tgt gtg tcc gtc tac aga tgt        837
Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys
                150                 155                 160

ggg ggt tgc tgc aat agt gag ggg ctg cag tgc atg aac acc agc acg        885
Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr
        165                 170                 175

agc tac ctc agc aag acg tta ttt gaa att aca gtg cct ctc tct caa        933
Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln
    180                 185                 190

ggc ccc aaa cca gta aca atc agt ttt gcc aat cac act tcc tgc cga        981
Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg
195                 200                 205                 210

tgc atg tct aaa ctg gat gtt tac aga caa gtt cat tcc att att aga        1029
Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg
                215                 220                 225

cgt tcc ctg cca gca aca cta cca cag tgt cag gca gcg aac aag acc        1077
Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr
                230                 235                 240

tgc ccc acc aat tac atg tgg aat aat cac atc tgc aga tgc ctg gct        1125
Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala
                245                 250                 255

cag gaa gat ttt atg ttt tcc tcg gat gct gga gat gac tca aca gat        1173
Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp
            260                 265                 270

gga ttc cat gac atc tgt gga cca aac aag gag ctg gat gaa gag acc        1221
Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr
275                 280                 285                 290
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tgt cag tgt gtc tgc aga gcg ggg ctt cgg cct gcc agc tgt gga ccc   1269
Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro
                295                 300                 305

cac aaa gaa cta gac aga aac tca tgc cag tgt gtc tgt aaa aac aaa   1317
His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys
                310                 315                 320

ctc ttc ccc agc caa tgt ggg gcc aac cga gaa ttt gat gaa aac aca   1365
Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr
                325                 330                 335

tgc cag tgt gta tgt aaa aga acc tgc ccc aga aat caa ccc cta aat   1413
Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn
                340                 345                 350

cct gga aaa tgt gcc tgt gaa tgt aca gaa agt cca cag aaa tgc ttg   1461
Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu
355                 360                 365                 370

tta aaa gga aag aag ttc cac cac caa aca tgc agc tgt tac aga cgg   1509
Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg
                375                 380                 385

cca tgt acg aac cgc cag aag gct tgt gag cca gga ttt tca tat agt   1557
Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser
                390                 395                 400

gaa gaa gtg tgt cgt tgt gtc cct tca tat tgg aaa aga cca caa atg   1605
Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro Gln Met
                405                 410                 415

agc taagattgta ctgttttcca gttcatcgat tttctattat ggaaaactgt        1658
Ser

gttgccacag tagaactgtc tgtgaacaga gagacccttg tgggtccatg ctaacaaaga 1718

caaaagtctg tctttcctga accatgtgga taactttaca gaaatggact ggagctcatc 1778

tgcaaaaggc ctcttgtaaa gactggtttt ctgccaatga ccaaacagcc aagattttcc 1838

tcttgtgatt tctttaaaag aatgactata taatttattt ccactaaaaa tattgtttct 1898

gcattcattt ttatagcaac aacaattggt aaaactcact gtgatcaata tttttatatc 1958

atgcaaaata tgtttaaaat aaaatgaaaa ttgtattat                        1997
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<210> 2
<211> 419
<212> PRT
<213> Homo sapiens

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Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe
             20                  25                  30

Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
             35                  40                  45
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Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
    50              55              60

Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
65              70              75              80

Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
            85              90              95

Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
            100             105             110

His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
    115             120             125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
    130             135             140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
145             150             155             160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
            165             170             175

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
            180             185             190

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
    195             200             205

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
210             215             220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
225             230             235             240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
            245             250             255

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
            260             265             270

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
    275             280             285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
    290             295             300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
305             310             315             320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
            325             330             335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
            340             345             350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
    355             360             365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
370             375             380
```

```
Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
385             390             395             400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
            405             410             415

Gln Met Ser


<210> 3
<211> 2029
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (411)..(1475)

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ttagagtgct ttctaatttc aggtagaaga catgtccacc ttctgattat ttttggagaa   180

catttgatt tttttcatct ctctctcccc accccctaaga ttgtgcaaaa aaagcgtacc   240

ttgcctaatt gaaataattt cattggattt tgatcagaac tgattatttg gttttctgtg   300

tgaagttttg aggtttcaaa ctttccttct ggagaatgcc ttttgaaaca attttctcta   360

gctgcctgat gtcaactgct tagtaatcag tggatattga aatattcaaa atg tac      416
                                                        Met Tyr
                                                         1

aga gag tgg gta gtg gtg aat gtt ttc atg atg ttg tac gtc cag ctg   464
Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val Gln Leu
         5              10              15

gtg cag ggc tcc agt aat gaa cat gga cca gtg aag cga tca tct cag   512
Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser Ser Gln
     20              25              30

tcc aca ttg gaa cga tct gaa cag cag atc agg gct gct tct agt ttg   560
Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser Ser Leu
 35              40              45              50

gag gaa cta ctt cga att act cac tct gag gac tgg aag ctg tgg aga   608
Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu Trp Arg
             55              60              65

tgc agg ctg agg ctc aaa agt ttt acc agt atg gac tct cgc tca gca   656
Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg Ser Ala
             70              75              80

tcc cat cgg tcc act agg ttt gcg gca act ttc tat gac att gaa aca   704
Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile Glu Thr
             85              90              95
```

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cta aaa gtt ata gat gaa gaa tgg caa aga act cag tgc agc cct aga    752
Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser Pro Arg
    100             105                 110

gaa acg tgc gtg gag gtg gcc agt gag ctg ggg aag agt acc aac aca    800
Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr Asn Thr
115             120                 125                 130

ttc ttc aag ccc cct tgt gtg aac gtg ttc cga tgt ggt ggc tgt tgc    848
Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly Cys Cys
                135                 140                 145

aat gaa gag agc ctt atc tgt atg aac acc agc acc tcg tac att tcc    896
Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr Ile Ser
                150                 155                 160

aaa cag ctc ttt gag ata tca gtg cct ttg aca tca gta cct gaa tta    944
Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro Glu Leu
            165                 170                 175

gtg cct gtt aaa gtt gcc aat cat aca ggt tgt aag tgc ttg cca aca    992
Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu Pro Thr
    180                 185                 190

gcc ccc cgc cat cca tac tca att atc aga aga tcc atc cag atc cct   1040
Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln Ile Pro
195                 200                 205                 210

gaa gaa gat cgc tgt tcc cat tcc aag aaa ctc tgt cct att gac atg   1088
Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile Asp Met
                215                 220                 225

cta tgg gat agc aac aaa tgt aaa tgt gtt ttg cag gag gaa aat cca   1136
Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu Asn Pro
                230                 235                 240

ctt gct gga aca gaa gac cac tct cat ctc cag gaa cca gct ctc tgt   1184
Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala Leu Cys
    245                 250                 255

ggg cca cac atg atg ttt gac gaa gat cgt tgc gag tgt gtc tgt aaa   1232
Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val Cys Lys
    260                 265                 270

aca cca tgt ccc aaa gat cta atc cag cac ccc aaa aac tgc agt tgc   1280
Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys Ser Cys
275                 280                 285                 290

ttt gag tgc aaa gaa agt ctg gag acc tgc tgc cag aag cac aag cta   1328
Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His Lys Leu
                295                 300                 305

ttt cac cca gac acc tgc agc tgt gag gac aga tgc ccc ttt cat acc   1376
Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe His Thr
                310                 315                 320

aga cca tgt gca agt ggc aaa aca gca tgt gca aag cat tgc cgc ttt   1424
Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys Arg Phe
            325                 330                 335
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cca aag gag aaa agg gct gcc cag ggg ccc cac agc cga aag aat cct   1472
Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys Asn Pro
    340             345             350

tga ttcagcgttc caagttcccc atccctgtca tttttaacag catgctgctt       1525
355

tgccaagttg ctgtcactgt ttttttccca ggtgttaaaa aaaaaatcca ttttacacag 1585

caccacagtg aatccagacc aaccttccat tcacaccagc taaggagtcc ctggttcatt 1645

gatggatgtc ttctagctgc agatgcctct gcgcaccaag gaatggagag gaggggaccc 1705

atgtaatcct tttgtttagt tttgtttttg ttttttggtg aatgagaaag gtgtgctggt 1765

catggaatgg caggtgtcat atgactgatt actcagagca gatgaggaaa actgtagtct 1825

ctgagtcctt tgctaatcgc aactcttgtg aattattctg attctttttt atgcagaatt 1885

tgattcgtat gatcagtact gactttctga ttactgtcca gcttatagtc ttccagttta 1945

atgaactacc atctgatgtt tcatatttaa gtgtatttaa agaaataaa caccattatt  2005

caagccaaaa aaaaaaaaaa aaaa                                         2029
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<210> 4
<211> 354
<212> PRT
<213> Homo sapiens

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Gln Leu Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser
                20              25              30

Ser Gln Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser
        35              40                  45

Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu
    50              55                  60

Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
65              70              75              80

Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
                85              90                  95

Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
            100             105             110

Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr
        115             120             125

Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
    130             135             140

Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr
145             150             155             160
```

```
Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro
                165             170             175

Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu
            180             185             190

Pro Thr Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln
            195             200             205

Ile Pro Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile
    210             215             220

Asp Met Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu
225             230             235             240

Asn Pro Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala
            245             250             255

Leu Cys Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val
            260             265             270

Cys Lys Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys
        275             280             285

Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His
    290             295             300

Lys Leu Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe
305             310             315             320

His Thr Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys
            325             330             335

Arg Phe Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys
            340             345             350

Asn Pro
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<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 5
ttggaggcct aggcttttgc   20

<210> 6
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 6
atactgtcgt cgtcccctca   20

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<210> 7
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 7
ggtagaagac cccaaggact tt                                        22


<210> 8
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 8
cgccattcgc cattcag                                              17


<210> 9
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 9
ctgcttactg gcttatcg                                             18


<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 10
cctgttctct gttatgttgc                                           20


<210> 11
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 11
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<210> 12
<211> 18
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 12
caagtgcatg gtggaagg                                              18


<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 13
tcgatccatg aactttctgc                                           20


<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
ttcgtttaac tcaagctgcc                                           20


<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15
gaccctggct ttactgctg                                            19


<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 16
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<210> 17
<211> 2679
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: chimeric
      sequence in which CMV promoter sequence is ligated
      to Homo sapien VEGF-C sequence

<400> 17
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agcccatata tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg 120

cccaacgacc cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata 180

gggactttcc attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta 240

catcaagtgt atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc 300

gcctggcatt atgcccagta catgacctta tgggactttc ctacttggca gtacatctac 360

gtattagtca tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga 420

tagcggtttg actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg 480

ttttggcacc aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg 540

caaatgggcg gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact 600

agagaaccca ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa 660

gctggctagc gtttaaactt aacccgcccc gcctctccaa aaagctacac cgacgcggac 720

cgcggcggcg tcctccctcg ccctcgcttc acctcgcggg ctccgaatgc ggggagctcg 780

gatgtccggt ttcctgtgag gcttttacct gacacccgcc gcctttcccc ggcactggct 840

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ggccaacctc aactcaagga cagaagagac tataaaattt gctgcagcac attataatac 1380

agagatcttg aaaagtattg ataatgagtg gagaaagact caatgcatgc cacgggaggt 1440

gtgtatagat gtggggaagg agtttggagt cgcgacaaac accttcttta aacctccatg 1500

tgtgtccgtc tacagatgtg ggggttgctg caatagtgag gggctgcagt gcatgaacac 1560

cagcacgagc tacctcagca agacgttatt tgaaattaca gtgcctctct ctcaaggccc 1620

caaaccagta acaatcagtt ttgccaatca cacttcctgc cgatgcatgt ctaaactgga 1680

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tgtttacaga caagttcatt ccattattag acgttccctg ccagcaacac taccacagtg 1740

tcaggcagcg aacaagacct gccccaccaa ttacatgtgg aataatcaca tctgcagatg 1800

cctggctcag gaagatttta tgttttcctc ggatgctgga gatgactcaa cagatggatt 1860

ccatgacatc tgtggaccaa acaaggagct ggatgaagag acctgtcagt gtgtctgcag 1920

agcggggctt cggcctgcca gctgtggacc ccacaaagaa ctagacagaa actcatgcca 1980

gtgtgtctgt aaaaacaaac tcttccccag ccaatgtggg gccaaccgag aatttgatga 2040

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